SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) ANMELDER:
(A) NAME: Vasopharm Biotech GmbH & Co. KG
(B) STREET: Leichtackerstr. 6
(C) CITY: Veitshöchheim
(D) STATE: Bayern
(E) COUNTRY: Deutschland
(F) POSTAL CODE: 97209

(ii) TITEL OF THE INVENTION: Isolated and purified human soluble guanylyl cyclase a1/ß1 (hsGCa1/ß1)

(iii) NUMBER OF SEQUENCES: 10

(iv) COMPUTER-READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) DATA TO SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3015 basepairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: doublestrand
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
CCCTTATGGC GATTGGGCGG CTGCAGAGAC CAGGACTCAG TTCCCCTGCC CTAGTCTGAG      60
CCTAGTGGGT GGGACTCAGC TCAGAGTCAG TTTTCCAGAA GCAGGTTTCA GTGCAGAGTT     120
TTCCTACACT TTTCCTGCGC TAGAGCAGCG AGCAGCCTGG AACAGACCCA GGCGGAGGAC     180
ACCTGTGGGG GAGGGAGCGC CTGGAGGAGC TTAGAGACCC CAGCCGGGCG TGATCTCACC     240
ATGTGCGGAT TTGCGAGGCG CGCCCTGGAG CTGCTAGAGA TCCGGAAGCA CAGCCCCGAG     300
GTGTGCGAAG CCACCAAGAC TGCGGCTCTT GGAGAAAGCG TGAGCAGGGG GCCACCGCGG     360
TCTCCGCGCC TGTCTGCACC CTGTCGCCTG AGCTGCCTGA CAGTGACAAT GACATCCCAG     420
TTACCAGTGT CCTTGAATTG ATAGTGGCTT CTGTTTGTCA GTCTCATATA AGAACTACAG     480
CTCATCAGGA GGAGATCGCA GCAGGGTAAG AGACACCAAC ACCATGTTCT GCACGAAGCT     540
CAAGGATCTC AAGATCACAG GAGAGTGTCC TTTCTCCTTA CTGGCACCAG GTCAAGTTCC     600
TAACGAGTCT TCAGAGGAGG CAGCAGGAAG CTCAGAGAGC TGCAAAGCAA CCGTGCCCAT     660
CTGTCAAGAC ATTCCTGAGA AGAACATACA AGAAAGTCTT CCTCAAAGAA AAACCAGTCG     720
GAGCCGAGTC TATCTTCACA CTTTGGCAGA GAGTATTTGC AAACTGATTT TCCCAGAGTT     780
TGAACGGCTG AATGTTGCAC TTCAGAGAAC ATTGGCAAAG CACAAAATAA AAGAAAGCAG     840
GAAATCTTTG GAAAGAGAAG ACTTTGAAAA AACAATTGCA GAGCAAGCAG TTGCAGCAGG     900
AGTTCCAGTG GAGGTTATCA AAGAATCTCT TGGTGAAGAG GTTTTTAAAA TATGTTACGA     960
GGAAGATGAA AACATCCTTG GGGTGGTTGG AGGCACCCTT AAAGATTTTT TAAACAGCTT    1020
CAGTACCCTT CTGAAACAGA GCAGCCATTG CCAAGAAGCA GGAAAAAGGG GCAGGCTTGA    1080
GGACGCCTCC ATTCTATGCC TGGATAAGGA GGATGATTTT CTACATGTTT ACTACTTCTT    1140
CCCTAAGAGA ACCACCTCCC TGATTCTTCC CGGCATCATA AAGGCAGCTG CTCACGTATT    1200
ATATGAAACG GAAGTGGAAG TGTCGTTAAT GCCTCCCTGC TTCCATAATG ATTGCAGCGA    1260
GTTTGTGAAT CAGCCCTACT TGTTGTACTC CGTTCACATG AAAAGCACCA AGCCATCCCT    1320
GTCCCCCAGC AAACCCCAGT CCTCGCTGGT GATTCCCACA TCGCTATTCT GCAAGACATT    1380
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TCCATTCCAT TTCATGTTTG ACAAAGATAT GACAATTCTG CAATTTGGCA ATGGCATCAG      1440
AAGGCTGATG AACAGGAGAG ACTTTCAAGG AAAGCCTAAT TTTGAAGAAT ACTTTGAAAT      1500
TCTGACTCCA AAAATCAACC AGACGTTTAG CGGGATCATG ACTATGTTGA ATATGCAGTT      1560
TGTTGTACGA GTGAGGAGAT GGGACAACTC TGTGAAGAAA TCTTCAAGGG TTATGGACCT      1620
CAAAGGCCAA ATGATCTACA TTGTTGAATC CAGTGCAATC TTGTTTTTGG GGTCACCCTG      1680
TGTGGACAGA TTAGAAGATT TTACAGGACG AGGGCTCTAC CTCTCAGACA TCCCAATTCA      1740
CAATGCACTG AGGGATGTGG TCTTAATAGG GGAACAAGCC CGAGCTCAAG ATGGCCTGAA      1800
GAAGAGGCTG GGGAAGCTGA AGGCTACCCT TGAGCAAGCC CACCAAGCCC TGGAGGAGGA      1860
GAAGAAAAAG ACAGTAGACC TTCTGTGCTC CATATTTCCC TGTGAGGTTG CTCAGCAGCT      1920
GTGGCAAGGG CAAGTTGTGC AAGCCAAGAA GTTCAGTAAT GTCACCATGC TCTTCTCAGA      1980
CATCGTTGGG TTCACTGCCA TCTGCTCCCA GTGCTCACCG CTGCAGGTCA TCACCATGCT      2040
CAATGCACTG TACACTCGCT TCGACCAGCA GTGTGGAGAG CTGGATGTCT ACAAGGTGGA      2100
GACCATTGGC GATGCCTATT GTGTAGCTGG GGGATTACAC AAAGAGAGTG ATACTCATGC      2160
TGTTCAGATA GCGCTGATGG CCCTGAAGAT GATGGAGCTC TCTGATGAAG TTATGTCTCC      2220
CCATGGAGAA CCTATCAAGA TGCGAATTGG ACTGCACTCT GGATCAGTTT TTGCTGGCGT      2280
CGTTGGAGTT AAAATGCCCC GTTACTGTCT TTTTGGAAAC AATGTCACTC TGGCTAACAA      2340
ATTTGAGTCC TGCAGTGTAC CACGAAAAAT CAATGTCAGC CCAACAACTT ACAGATTACT      2400
CAAAGACTGT CCTGGTTTCG TGTTTACCCC TCGATCAAGG GAGGAACTTC CACCAAACTT      2460
CCCTAGTGAA ATCCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACAAG GAACAAACTC      2520
AAAACCATGC TTCCAAAAGA AAGATGTGGA AGATGGCAAT GCCAATTTTT TAGGCAAAGC      2580
ATCAGGAATA GATTAGCAAC CTATATACCT ATTTATAAGT CTTTGGGGTT TGACTCATTG      2640
AAGATGTGTA GAGCCTCTGA AAGCACTTTA GGGATTGTAG ATGGCTAACA AGCAGTATTA      2700
AAATTTCAGG AGCCAAGTCA CAATCTTTCT CCTGTTTAAC ATGACAAAAT GTACTCACTT      2760
CAGTACTTCA GCTCTTCAAG AAAAAAAAAA AAACCTTAAA AAGCTACTTT TGTGGGAGTA      2820
TTTCTATTAT ATAACCAGCA CTTACTACCT GTACTCAAAA TTCAGCACCT TGTACATATA      2880
TCAGATAATT GTAGTCAATT GTACAAACTG ATGGAGTCAC CTGCAATCTC ATATCCTGGT      2940
GGAATGCCAT GGTTATTAAA GTGTGTTTGT GATAGTGTCG TCAAAAAAAA AAAAAAAAAA      3000
AAAAAAAAAA AAAAA                                                       3015
```

(2) DATA TO SEQ ID NO: 2:

(i) SEQUENCE CHARACERTISTICS:
(A) LENGTH: 695 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase a1 (hsGCa1))

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2:

```
Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro
  1               5                  10                  15
Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu
            20                  25                  30
Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln
        35                  40                  45
Asp Ile Pro Glu Lys Asn Ile Gln Glu Ser Leu Pro Gln Arg Lys Thr
    50                  55                  60
Ser Arg Ser Arg Val Tyr Leu His Thr Leu Ala Glu Ser Ile Cys Lys
65                  70                  75                  80
Leu Ile Phe Pro Glu Phe Glu Arg Leu Asn Val Ala Leu Gln Arg Thr
                85                  90                  95
Leu Ala Lys His Lys Ile Lys Glu Ser Arg Lys Ser Leu Glu Arg Glu
            100                 105                 110
Asp Phe Glu Lys Thr Ile Ala Glu Gln Ala Val Ala Ala Gly Val Pro
        115                 120                 125
Val Glu Val Ile Lys Glu Ser Leu Gly Glu Glu Val Phe Lys Ile Cys
    130                 135                 140
```

Tyr Glu Glu Asp Glu Asn Ile Leu Gly Val Val Gly Gly Thr Leu Lys
145 150 155 160
Asp Phe Leu Asn Ser Phe Ser Thr Leu Leu Lys Gln Ser Ser His Cys
165 170 175
Gln Glu Ala Gly Lys Arg Gly Arg Leu Glu Asp Ala Ser Ile Leu Cys
180 185 190
Leu Asp Lys Glu Asp Asp Phe Leu His Val Tyr Tyr Phe Phe Pro Lys
195 200 205
Arg Thr Thr Ser Leu Ile Leu Pro Gly Ile Ile Lys Ala Ala Ala His
210 215 220
Val Leu Tyr Glu Thr Glu Val Glu Val Ser Leu Met Pro Pro Cys Phe
2225 230 235 240
His Asn Asp Cys Ser Glu Phe Val Asn Gln Pro Tyr Leu Leu Tyr Ser
245 250 255
Val His Met Lys Ser Thr Lys Pro Ser Leu Ser Pro Ser Lys Pro Gln
260 265 270
Ser Ser Leu Val Ile Pro Thr Ser Leu Phe Cys Lys Thr Phe Pro Phe
275 280 285
His Phe Met Phe Asp Lys Asp Met Thr Ile Leu Gln Phe Gly Asn Gly
290 300 305
Ile Arg Arg Leu Met Asn Arg Arg Asp Phe Gln Gly Lys Pro Asn Phe
310 315 320 325
Glu Glu Tyr Phe Glu Ile Leu Thr Pro Lys Ile Asn Gln Thr Phe Ser
330 335 340
Gly Ile Met Thr Met Leu Asn Met Gln Phe Val Val Arg Val Arg Arg
345 350 355
Trp Asp Asn Ser Val Lys Lys Ser Ser Arg Val Met Asp Leu Lys Gly
360 365 370
Gln Met Ile Tyr Ile Val Glu Ser Ser Ala Ile Leu Phe Leu Gly Ser
375 380 385
Pro Cys Val Asp Arg Leu Glu Asp Phe Thr Gly Arg Gly Leu Tyr Leu
390 395 400 405
Ser Asp Ile Pro Ile His Asn Ala Leu Arg Asp Val Val Leu Ile Gly
410 415 420
Glu Gln Ala Arg Ala Gln Asp Gly Leu Lys Lys Arg Leu Gly Lys Leu
425 430 435
Lys Ala Thr Leu Glu Gln Ala His Gln Ala Leu Glu Glu Glu Lys Lys
440 445 450
Lys Thr Val Asp Leu Leu Cys Ser Ile Phe Pro Cys Glu Val Ala Gln
455 460 465
Gln Leu Trp Gln Gly Gln Val Val Gln Ala Lys Lys Phe Ser Asn Val
470 475 480 485
Thr Met Leu Phe Ser Asp Ile Val Gly Phe Thr Ala Ile Cys Ser Gln
490 495 500
Cys Ser Pro Leu Gln Val Ile Thr Met Leu Asn Ala Leu Tyr Thr Arg
505 510 515
Phe Asp Gln Gln Cys Gly Glu Leu Asp Val Tyr Lys Val Glu Thr Ile
520 525 530
Gly Asp Ala Tyr Cys Val Ala Gly Gly Leu His Lys Glu Ser Asp Thr
535 540 545
His Ala Val Gln Ile Ala Leu Met Ala Leu Lys Met Met Glu Leu Ser
550 555 560 565
Asp Glu Val Met Ser Pro His Gly Glu Pro Ile Lys Met Arg Ile Gly
570 575 580
Leu His Ser Gly Ser Val Phe Ala Gly Val Val Gly Val Lys Met Pro
585 590 595
Arg Tyr Cys Leu Phe Gly Asn Asn Val Thr Leu Ala Asn Lys Phe Glu
600 605 610
Ser Cys Ser Val Pro Arg Lys Ile Asn Val Ser Pro Thr Thr Tyr Arg
615 620 625
Leu Leu Lys Asp Cys Pro Gly Phe Val Phe Thr Pro Arg Ser Arg Glu

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630                 635                 640                 645
Glu Leu Pro Pro Asn Phe Pro Ser Glu Ile Pro Gly Ile Cys His Phe
                650                 655                 660
Leu Asp Ala Tyr Gln Gln Gly Thr Asn Ser Lys Pro Cys Phe Gln Lys
            665                 670                 675
Lys Asp Val Glu Asp Gly Asn Ala Asn Phe Leu Gly Lys Ala Ser Gly
        680                 685                 690
Ile Asp
    695
```

(2) DATA TO SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2443 basepairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: doublestrand
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
CCCCCCCCCG CCGCTGCCGC CTCTGCCTGG GTCCCTTCGG CCGTACCTCT GCGTGGGGGC   60
TGCCTCCCCG GCTCCCGGTG CAGACACCAT GTACGGATTT GTGAATCACG CCCTGGAGTT  120
GCTGGTGATC CGCAATTACG GCCCCGAGGT GTGGGAAGAC ATCAAAAAAG AGGCACAGTT  180
AGATGAAGAA GGACAGTTTC TTGTCAGAAT AATATATGAT GACTCCAAAA CTTATGATTT  240
GGTTGCTGCT GCAAGCAAAG TCCTCAATCT CAATGCTGGA GAAATCCTCC AAATGTTTGG  300
GAAGATGTTT TTCGTCTTTT GCCAAGAATC TGGTTATGAT ACAATCTTGC GTGTCCTGGG  360
CTCTAATGTC AGAGAATTTC TACAGAACCT TGATGCTCTG CACGACCACC TTGCTACCAT  420
CTACCCAGGA ATGCGTGCAC CTTCCTTTAG GTGCACTGAT GCAGAAAAGG GCAAAGGACT  480
CATTTTGCAC TACTACTCAG AGAGAGAAGG ACTTCAGGAT ATTGTCATTG GAATCATCAA  540
AACAGTGGCA CAACAAATCC ATGGCACTGA AATAGACATG AAGGTTATTC AGCAAAGAAA  600
TGAAGAATGT GATCATACTC AATTTTTAAT TGAAGAAAAA GAGTCAAAAG AAGAGGATTT  660
TTATGAAGAT CTTGACAGAT TTGAAGAAAA TGGTACCCAG GAATCACGCA TCAGCCCATA  720
TACATTCTGC AAAGCTTTTC CTTTTCATAT AATATTTGAC CGGGACCTAG TGGTCACTCA  780
GTGTGGCAAT GCTATATACA GAGTTCTCCC CCAGCTCCAG CCTGGGAATT GCAGCCTTCT  840
GTCTGTCTTC TCGCTGGTTC GTCCTCATAT TGATATTAGT TTCCATGGGA TCCTTTCTCA  900
CATCAATACT GTTTTTGTAT TGAGAAGCAA GGAAGGATTG TTGGATGTGG AGAAATTAGA  960
ATGTGAGGAT GAACTGACTG GGACTGAGAT CAGCTGCTTA CGTCTCAAGG GTCAAATGAT 1020
CTACTTACCT GAAGCAGATA GCATACTTTT TCTATGTTCA CCAAGTGTCA TGAACCTGGA 1080
CGATTTGACA AGGAGAGGGC TGTATCTAAG TGACATCCCT CTGCATGATG CCACGCGCGA 1140
TCTTGTTCTT TTGGGAGAAC AATTTAGAGA GGAATACAAA CTCACCCAAG AACTGGAAAT 1200
CCTCACTGAC AGGCTACAGC TCACGTTAAG AGCCCTGGAA GATGAAAAGA AAAAGACAGA 1260
CACATTGCTG TATTCTGTCC TTCCTCCGTC TGTTGCCAAT GAGCTGCGGC ACAAGCGTCC 1320
AGTGCCTGCC AAAAGATATG ACAATGTGAC CATCCTCTTT AGTGGCATTG TGGGCTTCAA 1380
TGCTTTCTGT AGCAAGCATG CATCTGGAGA AGGAGCCATG AAGATCGTCA ACCTCCTCAA 1440
CGACCTCTAC ACCAGATTTG ACACACTGAC TGATTCCCGG AAAAACCCAT TTGTTTATAA 1500
GGTGGAGACT GTTGGTGACA AGTATATGAC AGTGAGTGGT TTACCAGAGC CATGCATTCA 1560
CCATGCACGA TCCATCTGCC ACCTGGCCTT GGACATGATG GAAATTGCTG GCCAGGTTCA 1620
AGTAGATGGT GAATCTGTTC AGATAACAAT AGGGATACAC ACTGGAGAGG TAGTTACAGG 1680
TGTCATAGGA CAGCGGATGC CTCGATACTG TCTTTTTGGG AATACTGTCA ACCTCACAAG 1740
CCGAACAGAA ACCACAGGAG AAAAGGGAAA AATAAATGTG TCTGAATATA CATACAGATG 1800
TCTTATGTCT CCAGAAAATT CAGATCCACA ATTCCACTTG GAGCACAGAG GCCCAGTGTC 1860
CATGAAGGGC AAAAAAGAAC CAATGCAAGT TTGGTTTCTA TCCAGAAAAA ATACAGGAAC 1920
AGAGGAAACA AAGCAGGATG ATGACTGAAT CTTGGATTAT GGGGTGAAGA GGAGTACAGA 1980
CTAGGTTCCA GTTTTCTCCT AACACGTGCC AAGCCCAGGA GCAGTTCTTC CCTATGGATA 2040
CAGATTTTCT TTTGTCCTTG TCCATTACCC CAAGACTTTC TTCTAGATAT ATCTCTCACT 2100
ATCCGTTATT CAACCTTAGC TCTGCTTTCT ATTACTTTTT AGGCTTTAGT ATATTATCTA 2160
AAGTTTGGCT TTTGATGTGG ATGATGTGAG CTTCATGTGT CTTAAAATCT ACTACAAGCA 2220
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TTACCTAACA TGGTGATCTG CAAGTAGTAG GCACCCAATA AATATTTGTT GAATTTAGTT      2280
AAATGAAACT GAACAGTGTT TGGCCATGTG TATATTTATA TCATGTTTAC CAAATCTGTT      2340
TAGTGTTCCA CATATATGTA TATGTATATT TTAATGACTA TAATGTAATA AAGTTTATAT      2400
CATGTTGGTG TATATCATTA TAGAAATCAT TTTCTAAAGG AGT                        2443
```

(2) DATA TO SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 619 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase b1 (hsGCb1))

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 4:

```
Met Tyr Gly Phe Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn
  5                  10                  15
Tyr Gly Pro Glu Val Trp Glu Asp Ile Lys Lys Glu Ala Gln Leu Asp
            20                  25                  30
Glu Glu Gly Gln Phe Leu Val Arg Ile Ile Tyr Asp Asp Ser Lys Thr
        35                  40                  45
Tyr Asp Leu Val Ala Ala Ala Ser Lys Val Leu Asn Leu Asn Ala Gly
    50                  55                  60
Glu Ile Leu Gln Met Phe Gly Lys Met Phe Phe Val Phe Cys Gln Glu
65                  70                  75                  80
Ser Gly Tyr Asp Thr Ile Leu Arg Val Leu Gly Ser Asn Val Arg Glu
                85                  90                  95
Phe Leu Gln Asn Leu Asp Ala Leu His Asp His Leu Ala Thr Ile Tyr
            100                 105                 110
Pro Gly Met Arg Ala Pro Ser Phe Arg Cys Thr Asp Ala Glu Lys Gly
        115                 120                 125
Lys Gly Leu Ile Leu His Tyr Tyr Ser Glu Arg Glu Gly Leu Gln Asp
    130                 135                 140
Ile Val Ile Gly Ile Ile Lys Thr Val Ala Gln Gln Ile His Gly Thr
145                 150                 155                 160
Glu Ile Asp Met Lys Val Ile Gln Gln Arg Asn Glu Glu Cys Asp His
                165                 170                 175
Thr Gln Phe Leu Ile Glu Glu Lys Glu Ser Lys Glu Glu Asp Phe Tyr
            180                 185                 190
Glu Asp Leu Asp Arg Phe Glu Glu Asn Gly Thr Gln Glu Ser Arg Ile
        195                 200                 205
Ser Pro Tyr Thr Phe Cys Lys Ala Phe Pro Phe His Ile Ile Phe Asp
    210                 215                 220
Arg Asp Leu Val Val Thr Gln Cys Gly Asn Ala Ile Tyr Arg Val Leu
225                 230                 235                 240
Pro Gln Leu Gln Pro Gly Asn Cys Ser Leu Leu Ser Val Phe Ser Leu
                245                 250                 255
Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser His Ile
            260                 265                 270
Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu
        275                 280                 285
Lys Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu
    290                 295                 300
Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu
305                 310                 315                 320
Phe Leu Cys Ser Pro Ser Val Met Asn Leu Asp Asp Leu Thr Arg Arg
                325                 330                 335
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Gly Leu Tyr Leu Ser Asp Ile Pro Leu His Asp Ala Thr Arg Asp Leu
            340                 345                 350
Val Leu Leu Gly Glu Gln Phe Arg Glu Glu Tyr Lys Leu Thr Gln Glu
        355                 360                 365
Leu Glu Ile Leu Thr Asp Arg Leu Gln Leu Thr Leu Arg Ala Leu Glu
    370                 375                 380
Asp Glu Lys Lys Lys Thr Asp Thr Leu Leu Tyr Ser Val Leu Pro Pro
385                 390                 395                 400
Ser Val Ala Asn Glu Leu Arg His Lys Arg Pro Val Pro Ala Lys Arg
                405                 410                 415
Tyr Asp Asn Val Thr Ile Leu Phe Ser Gly Ile Val Gly Phe Asn Ala
            420                 425                 430
Phe Cys Ser Lys His Ala Ser Gly Glu Gly Ala Met Lys Ile Val Asn
        435                 440                 445
Leu Leu Asn Asp Leu Tyr Thr Arg Phe Asp Thr Leu Thr Asp Ser Arg
    450                 455                 460
Lys Asn Pro Phe Val Tyr Lys Val Glu Thr Val Gly Asp Lys Tyr Met
465                 470                 475                 480
Thr Val Ser Gly Leu Pro Glu Pro Cys Ile His His Ala Arg Ser Ile
                485                 490                 495
Cys His Leu Ala Leu Asp Met Met Glu Ile Ala Gly Gln Val Gln Val
            500                 505                 510
Asp Gly Glu Ser Val Gln Ile Thr Ile Gly Ile His Thr Gly Glu Val
        515                 520                 525
Val Thr Gly Val Ile Gly Gln Arg Met Pro Arg Tyr Cys Leu Phe Gly
    530                 535                 540
Asn Thr Val Asn Leu Thr Ser Arg Thr Glu Thr Thr Gly Glu Lys Gly
545                 550                 555                 560
Lys Ile Asn Val Ser Glu Tyr Thr Tyr Arg Cys Leu Met Ser Pro Glu
                565                 570                 575
Asn Ser Asp Pro Gln Phe His Leu Glu His Arg Gly Pro Val Ser Met
            580                 585                 590
Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn
        595                 600                 605
Thr Gly Thr Glu Glu Thr Lys Gln Asp Asp Asp
    610                 615
```

(2) DATA TO SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (amino acids 634-647 of hsGCa1)

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 5:

```
Phe Thr Pro Arg Ser Arg Glu Glu Leu Pro Pro Asn Phe Pro
                5                   10
```

(2) DATA TO SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (amino acids 593-614 of hsGCb1)

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 6:

Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn
5 10 15
Thr Gly Thr Glu Glu Thr
20

(2) DATA TO SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 basepairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single strans
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 7:

AAAAGGATCC ATGTTCTGCA CGAAGCTC 28

2) DATA TO SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 basepairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single strans
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 8:

ATTATGGAAG CAGGGAGG 18

2) DATA TO SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 basepairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single strans
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 9:

AAAAGGATCC ATGTACGGAT TTGTGAAT 28

2) DATA TO SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 basepairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single strans
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 10:

ATGCGTGATT CCTGGGTACC 20